



SEQUENCE LISTING

<110> KIKUTANI, HITOSHI KUMANOGOH, ATSUSHI HORI, AKIRA

<120> SCREENING METHOD USING CD100

<130> 46342/56,721

<140> 10/009,330

<141> 2001-12-03

<150> PCT/JP00/03558

<151> 2000-06-01

<150> JP 157111/1999

<151> 1999-06-03

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 861

<212> PRT

<213> Mus sp.

<400> 1

Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu Ala Leu Val Val 1 5 10 15

Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro Arg Leu Thr Trp 20 25 30

Glu His Gly Glu Val Gly Leu Val Gln Phe His Lys Pro Gly Ile Phe 35 40 45

Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp Thr Leu Tyr Val 50 55 60

Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu 65 70 75 80

Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ser Lys 85 90 95

Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile 100 105 110

Arg Val Leu Gln Pro Leu Ser Ser Thr Ser Leu Tyr Val Cys Gly Thr 115 120 125

Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu Thr Ser Phe Lys 130 135 140

Phe Leu Gly Lys Ser Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro 145 150 155 160



- Ala His Ser Tyr Thr Ser Val Met Val Gly Gly Glu Leu Tyr Ser Gly 165 170 175
- Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
- Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu 195 200 205
- Pro Ser Phe Val Phe Ala Asp Val Île Gln Lys Ser Pro Asp Gly Pro 210 215 220
- Glu Gly Glu Asp Asp Lys Val Tyr Phe Phe Phe Thr Glu Val Ser Val 225 230 235 240
- Glu Tyr Glu Phe Val Phe Lys Leu Met Ile Pro Arg Val Ala Arg Val 245 250 255
- Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr 260 265 270
- Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Lys Pro Asp Ser Gly Leu 275 280 285
- Val Phe Asn Ile Leu Gln Asp Val Phe Val Leu Arg Ala Pro Gly Leu 290 295 300
- Lys Glu Pro Val Phe Tyr Ala Val Phe Thr Pro Gln Leu Asn Asn Val 305 310 315 320
- Gly Leu Ser Ala Val Cys Ala Tyr Thr Leu Ala Thr Val Glu Ala Val 325 330 335
- Phe Ser Arg Gly Lys Tyr Met Gln Ser Ala Thr Val Glu Gln Ser His 340 345 350
- Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Thr Pro Arg Pro Gly 355 360 365
- Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu 370 375 380
- Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met 385 390 395 400
- Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Lys Leu Ile Lys Lys 405 410 415
- Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp 420 425 430
- Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp Arg Gly Ala Leu 435 440 445
- His Lys Ala Val Ile Leu Thr Lys Glu Val His Val Ile Glu Glu Thr 450 455 460



Gln Leu Phe Arg Asp Phe Glu Pro Val Leu Thr Leu Leu Leu Ser Ser 470 Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val 490 Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser Cys Glu Asp Cys Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Ala Ile Lys Ala 520 Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg Gly Trp Ile Gln Asp Met Ser Gly Asp Thr Ser Ser Cys Leu Asp Lys Ser Lys Glu Ser Phe Asn Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys Phe Gln Lys Ser Asn Leu Ala Arg Val Val Trp Lys Phe Gln Asn Gly Glu Leu Lys Ala Ala Ser Pro Lys Tyr Gly Phe Val Gly Arg Lys His 600 Leu Leu Ile Phe Asn Leu Ser Asp Gly Asp Ser Gly Val Tyr Gln Cys Leu Ser Glu Glu Arg Val Arg Asn Lys Thr Val Ser Gln Leu Leu Ala Lys His Val Leu Glu Val Lys Met Val Pro Arg Thr Pro Pro Ser Pro 650 Thr Ser Glu Asp Val Gln Thr Glu Gly Ser Lys Ile Thr Ser Lys Met 665 Pro Val Gly Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Leu Trp Ala Thr Ser Pro Arg Ala Ala Thr Leu Pro Pro Lys Ser Ser Ser Gly Thr Ser Cys Glu Pro Lys Met Val Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Val Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu Met 730 Ser Leu Leu Phe Ile Phe Val Leu Phe Leu Cys Leu Phe Ser Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Gly Gln Cys Leu Lys Phe Arg Ser



Ala Leu Leu Leu Gly Lys Lys Thr Pro Lys Ser Asp Phe Ser Asp Leu 770 775 775 8 8 8 9 Phe Ser Asp Leu 780 780 780 780 780 780 780 800

Gln Asn Gly Asp His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr 805 810 815

Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser 820 825 830

Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys 835 840 845

Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp 850 855 860

<210> 2 <211> 2769 <212> DNA

<213> Mus sp.

<400> 2

gaatteggea egaggeeate catgtgtgee egttgetgaa ggeeteggtg geecetgeee 60 atgaggatgt gtgcccccgt tagggggctg ttcttggccc tggtggtagt gttgagaacc 120 geggtggcat ttgcacctgt geeteggete acetgggaac atggagaggt aggtetggtg 180 cagtttcaca agccaggcat ctttaactac teggeettge tgatgagtga ggacaaagae 240 actetqtatq taqqcqccq qqaaqcaqtc tttgcagtga atgcgctgaa catctctgag 300 aagcaacatg aggtatattg gaaggtotot gaagacaaaa aatocaagtg tgcagagaag 360 gggaaatcaa agcagacgga atgcctaaac tacattcgag tactacagcc actaagcagc 420 acttccctct atgtgtgtgg gaccaatgcg ttccagccca cctgtgacca cctgaacttg 480 acateettea agtitetggg gaaaagtgaa gatggcaaag gaagatgeee ettegaeeee 540 geceacaget acacateagt catggttggg ggegagetet actetgggae gteetataat 600 ttottgggca gtgaacccat catctctcga aactcttccc acagtccctt gaggacggag 660 tatgccatcc cgtggctgaa cgagcctagc ttcgtctttg ctgacgtgat ccagaaaagc 720 ccagatggtc cggagggtga agatgacaag gtctacttct tttttacgga ggtatccgtg 780 gagtacgaat tegtetteaa gttgatgate eegegagttg eeagggtgtg eaagggegae 840 cagggeggee tgeggaettt gcaaaaaaag tggaeeteet teetaaagge caggetgate 900 tgctccaagc cagacagtgg cctggtcttc aacatacttc aggatgtgtt tgtgctgagg 960 gccccgggcc tcaaggagcc tgtgttctat gcggtcttca ccccacagct gaacaatgtg 1020 ggtctgtcag cggtgtgcgc ctacacactg gccacggtgg aggcagtctt ctcccgtgga 1080 aagtacatgc agagtgccac agtggagcag tctcacacca agtgggtgcg ctacaatggc 1140 ccagtgccca ctccccgacc tggagcgtgt atcgacagtg aggcccgggc agccaactac 1200 accageteet tgaateteee agacaaaaca etgeagtttg taaaagacea eeetttgatg 1260 gatgactcag tgaccccgat agacaacaga cccaagctga tcaaaaaaaga tgtaaactac 1320 acccagatag tggtagacag gacccaggcc ctggatggga ctttctacga cgtcatgttc 1380 atcagcacag accggggage tetgcataaa geagteatee teacaaaaga ggtgcatgte 1440 ategaggaga cecaactett eegggactet gaaceggtee taactetget getategtea 1500 aagaagggga ggaagtttgt ctatgcaggc tccaactctg gagtggtcca agcgccctg 1560 gcattctgcg aaaagcacgg tagctgtgaa gactgtgtgt tagcacggga cccctactgt 1620 gcctggagcc cagccatcaa ggcctgtgtt accctgcacc aggaagaggc ctccagcagg 1680 ggctggattc aggacatgag cggtgacaca tcctcatgcc tggataagag taaagaaagt 1740 ttcaaccage attitttcaa geacggegge acageggaac teaaatgitt ecaaaagtee 1800 aacctagccc gggtggtatg gaagttccag aatggcgagt tgaaggccgc aagtcccaag 1860 tacggetttg tgggeaggaa geacetgete atetteaace tgteggaegg agacagegge 1920 gtgtaccagt gcctgtcaga ggaaagggtg aggaataaaa cggtctccca gctgctggcc 1980

1



aagcacg	ttc	tggaagtgaa	gatggtacct	cggacccccc	cctcacctac	ctcagaggat	2040
						ccaggggtcc	
						acctcccaag	
tectect	ccg	gcacatcctg	tgaaccaaag	atggtcatca	acacggtccc	ccagctccac	2220
						tctcctcctc	
						ctacctgccc	
ggacagt	gct	taaaattccg	ctcagccctg	ctgcttggaa	agaaaacacc	caagtcagac	2400
						cttctcccag	
						gcaggacacc	
						actctctgcc	
						tgctgacggg	
						gttgtgttga	
						teceetttt	
ctctggt	tt						2769

<210> 3 <211> 862 <212> PRT

<213> Homo sapiens

<400>3

Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val 1 5 .15

Met Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp
20 25 30

Glu His Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr 35 40 45

Asn Tyr Ser Ala Leu Leu Ser Glu Asp Lys Asp Thr Leu Tyr Ile
50 55 60

Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu 65 70 75 80

Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys 85 90 95

Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile 100 105 110

Arg Val Leu Gln Pro Leu Ser Ala Thr Ser Leu Tyr Val Cys Gly Thr 115 120 125

Asn Ala Phe Gln Pro Ala Cys Asp His Leu Asn Leu Thr Ser Phe Lys 130 135 140

Phe Leu Gly Lys Asn Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro 145 150 155 160

Ala His Ser Tyr Thr Ser Val Met Val Asp Gly Glu Leu Tyr Ser Gly
165 170 175

Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Île Ser Arg Asn Ser 180 185 190



- Ser His S r Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu 200 Pro Ser Phe Val Phe Ala Asp Val Ile Arg Lys Ser Pro Asp Ser Pro Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val Ser Val 230 235 Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg Val 250 Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu 280 Val Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val 315 Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val 330 325 Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His 345 Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu 375 380 Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys 405 Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
- His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr
 450
 445
 460

Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu

- Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser 465 470 475 480
- Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val 485 490 495



Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr 520 Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn Leu Leu Île Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala 630 Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln 680 Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu 730 Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu Phe Phe 740 Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg 760 Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser



Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu 805 810 815

Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp
820 825 830

Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val 835 840 845

Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp . 850 860

<21.0> 4

<211> 4157

<212> DNA

<213> Homo sapiens

<400> 4

etgageegea tetgeaatag cacaettgee eggeeacetg etgeegtgag cetttgetge 60 tgaagcccct ggggtcgcct ctacctgatg aggatgtgca cccccattag ggggctgctc 120 atggeeettg eagtgatgtt tgggaeageg atggeatttg eacceatace eeggateace 180 tgggagcaca gagaggtgca cetggtgcag tttcatgage cagacateta caactactea 240 geettgetge tgagegagga caaggacaee ttgtacatag gtgeeeggga ggeggtette 300 gctgtgaacg cactcaacat ctccgagaag cagcatgagg tgtattggaa ggtctcagaa 360 gacaaaaaag caaaatgtgc agaaaagggg aaatcaaaac agacagagtg cctcaactac 420 atcegggtge tgcagecact cagegecact tecetttaeg tgtgtgggae caaegeatte 480 cagccggcct gtgaccacct gaacttaaca tcctttaagt ttctggggaa aaatgaagat 540 ggcaaaggaa gatgtccctt tgacccagca cacagctaca catccgtcat ggttgatgga 600 gaactttatt eggggaegte gtataatttt ttgggaagtg aacccatcat etceegaaat 660 tétteccaca gteetetgag gacagaatat geaateeett ggetgaaega geetagtéte 720 gtgtttgctg acgtgatccg aaaaagccca gacagccccg acggcgagga tgacagggtc 780 tacttettet teaeggaggt gtetgtggag tatgagtttg tgtteagggt getgateeca 840 cggatagcaa gagtgtgcaa gggggaccag ggcggcctga ggaccttgca gaagaaatgg 900 acctectice tgaaageeeg acteatetge teeeggeeag acageggett ggtetteaat 960 gtgctgcggg atgtcttcgt gctcaggtcc ccgggcctga aggtgcctgt gttctatgca 1020 ctcttcaccc cacagetgaa caacgtgggg etgteggeag tgtgegeeta caacetgtee 1080 acagoogagg aggtottoto ocaogggaag tacatgoaga gcaccacagt ggagoagtoo 1140 cacaccaagt gggtgcgcta taatggcccg gtacccaagc cgcggcctgg agcgtgcatc 1200 gacagogagg caogggoogo caactacaco agotoottga atttgocaga caagaogotg 1260 cagttcgtta aagaccaccc tttgatggat gactcggtaa ccccaataga caacaggccc 1320 aggttaatca agaaagatgt gaactacacc cagatcgtgg tggaccggac ccaggccctg 1380 gatgggactg tetatgatgt catgtttgte ageacagace ggggagetet geacaaagee 1440 atcagecteg ageaegetgt teacateate gaggagaeee agetetteea ggaetttgag 1500 ccagtccaga ccctgctgct gtcttcaaag aagggcaaca ggtttgtcta tgctggctct 1560 aactegggeg tggtecagge ceegetggee ttetgtggga ageaeggeae etgegaggae 1620 tgtgtgctgg cgcgggaccc ctactgcgcc tggagcccgc ccacagcgac ctgcgtggct 1680 ctgcaccaga ccgagagccc cagcaggggt ttgattcagg agatgagcgg cgatgcttct 1740 gtgtgcccgg ataaaagtaa aggaagttac cggcagcatt ttttcaagca cggtggcaca 1800 geggaactga aatgeteeca aaaatecaac etggeeeggg tettttggaa gtteeagaat 1860 ggcgtgttga aggccgagag ccccaagtac ggtcttatgg gcagaaaaaa cttgctcatc 1920 ttcaacttgt cagaaggaga cagtggggtg taccagtgcc tgtcagagga gagggttaag 1980 aacaaaacgg tetteeaagt ggtegeeaag eacgteetgg aagtgaaggt ggtteeaaag 2040 cccgtagtgg ccccacctt gtcagttgtt cagacagaag gtagtaggat tgccaccaaa 2100 gtgttggtgg catccaccca agggtcttct cccccaaccc cagccgtgca ggccacctcc 2160 teeggggeea teaccettee teecaageet gegéeeaceg geacateetg egaaceaaag 2220 atogtoatoa acaeggteee eeageteeae teggagaaaa eeatgtatet taagteeage 2280 gacaaccgcc tecteatgte cetetteete ttettetttg ttetetteet etgeetettt 2340



```
ttctacaact gctataaggg atacctgccc agacagtgct tgaaattccg ctcggcccta 2400
ctaattggga agaagaagcc caagtcagat ttctgtgacc gtgagcagag cctgaaggag 2460
acgttagtag agccagggag cttctcccag cagaatgggg agcaccccaa gccagccctg 2520
gacaccggct atgagaccga gcaagacacc atcaccagca aagtccccac ggatagggag 2580
gactcacaga ggatcgacga cetttetgee agggacaage cetttgaegt caagtgtgag 2640
ctgaagttcg ctgactcaga cgcagatgga gactgaggcc ggctgtgcat ccccgctggt 2700
gcctcggctg cgacgtgtcc aggcgtggag agttttgtgt ttctcctgtt cagtatccga 2760
gtctcgtgca gtgctgcgta ggttagcccg catcgtgcag acaacctcag tcctcttgtc 2820
tattttctct tgggttgagc ctgtgacttg gtttctcttt gtccttttgg aaaaatgaca 2880
aqcattqcat cccaqtcttq tqttccgaag tcagtcggag tacttgaaga aggcccacgg 2940
geggeaegga gtteetgage cetttetgta gtgggggaaa ggtggetgga cetetgttgg 3000
ctgagaagag catcccttca gcttcccctc cccgtagcag ccactaaaag attatttaat 3060
tecagattgg aaatgacatt ttagtttate agattggtaa ettategeet gttgtecaga 3120
ttqqcacqaa ccttttcttc cacttaatta tttttttagg attttgcttt gattgtgttt 3180
atgtcatggg tcattttttt ttagttacag aagcagttgt gttaatattt agaagaagat 3240
gtatatette cagattttgt tatatatttg gcataaaata cggcttacgt tgcttaagat 3300
teteagggat aaaetteett tigetaaaig eattetitet getittagaa aigtagaeat 3360
aaacacteee eggageeeae teacettttt tetttttett tittttttt taactttatt 3420
cettgaggga agcattgttt ttggagagat tttetttetg taettegttt taettttett 3480
tttttttaac ttttactctc tcgaagaaga ggaccttccc acatccacga ggtgggtttt 3540
gagcaaggga aggtagcctg gatgagctga gtggagccag gctggcccag agctgagatg 3600
ggagtgeggt acaatetgga geceacaget gteggteaga aceteetgtg agacagatgg 3660
aacetteada agggegeett tggttetetg aacateteet ttetettett getteaattg 3720
cttacccact gcctgcccag actttctatc cagcctcact gagctgccca ctactggaag 3780
ggaactgggc eteggtggee ggggeegega getgtgaeea eageaceete aageataegg 3840
cgctgttcct gccactgtcc tgaagatgtg aatgggtggt acgatttcaa cactggttaa 3900
tttcacactc catctccccg ctttgtaaat acccatcggg aagagacttt ttttccatgg 3960
tgaagagcaa taaactctgg atgtttgtgc gcgtgtgtgg acagtcttat cttccagcat 4020
gataggattt gaccattttg gtgtaaacat ttgtgtttta taagatttac cttgttttta 4080
tttttctact ttgaattgta tacatttgga aagtacccaa ataaatgaga agcttctatc 4140
cttaaaaaaa aaaaaaa
```

```
<210> 5
<211> 361
<212> PRT
```

<213> Mus sp.

Leu Lys Asn Ser Ala Ser Asn His Leu Gly Gln Asp Cys Glu Ala Tyr 20 25 30

Glu Asp Gly Glu Leu Thr Tyr Glu Asn Val Gln Val Ser Pro Val Pro
35 40 45

Gly Gly Pro Pro Gly Leu Ala Ser Pro Ala Leu Ala Asp Lys Ala Gly
50 55 60

Val Gly Ser Glu Gln Pro Thr Ala Thr Trp Ser Ser Val Asn Ser Ser 65 70 75 80

Ala Leu Arg Gln Ile Pro Arg Cys Pro Thr Val Cys Leu Gln Tyr Phe 85 90 95



Leu Leu Gly Leu Leu Val Ser Cys Leu Met Leu Gly Val Ala Val Ile 105 Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Arg Gln Phe Gln Glu Gly 120 Thr Arg Ile Trp Glu Ala Thr Asn Ser Ser Leu Gln Gln Gln Leu Arg Glu Lys Ile Ser Gln Leu Gly Gln Lys Glu Val Glu Leu Gln Lys Ala 155 Arg Lys Glu Leu Ile Ser Ser Gln Asp Thr Leu Gln Glu Lys Gln Arg 165 170 Thr His Glu Asp Ala Glu Gln Gln Leu Gln Ala Cys Gln Ala Glu Arg Ala Lys Thr Lys Glu Asn Leu Lys Thr Glu Glu Glu Arg Arg Asp Leu Asp Gln Arg Leu Thr Ser Thr Arg Glu Thr Leu Arg Arg Phe Phe 215 Ser Asp Ser Ser Asp Thr Cys Cys Pro Cys Gly Trp Ile Pro Tyr Gln 230 Glu Arg Cys Phe Tyr Ile Ser His Thr Leu Gly Ser Leu Glu Glu Ser Gln Lys Tyr Cys Thr Ser Leu Ser Ser Lys Leu Ala Ala Phe Asp Glu Pro Ser Lys Tyr Tyr Tyr Glu Tyr Leu Ser Asp Ala Pro Gln Val Ser 280 Leu Pro Ser Gly Leu Glu Glu Leu Leu Asp Arg Ser Lys Ser Tyr Trp 300 Ile Gln Met Ser Lys Lys Trp Arg Gln Asp Ser Asp Ser Gln Ser Arg 315 His Cys Val Arg Ile Lys Thr Tyr Tyr Gln Lys Trp Glu Arg Thr Ile 330 Ser Lys Cys Ala Glu Leu His Pro Cys Ile Cys Glu Ser Glu Ala Phe

355 360

Arg Phe Pro Asp Gly Ile Asn Leu Asn

<210> 6 <211> 1337 <212> DNA <213> Mus sp.



```
<400> 6
tggaagactg tgaagcagag gcgcccaggg ctatggctga cgctatcacg tatgcagacc 60
tgcgctttgt gaaagtgccc ctgaagaaca gcgcatctaa ccatctagga caggactgtg 120
aggectatga agatggggaa eteacetacg agaatgtgea agtgteteca gteecaggag 180
ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagcaac 240
caactgogac ctggagetet gtgaactcgt ctgeteteag geagatteee egetgteeta 300
cagtetgett geaatactte ttgettggee ttetegtgte etgtetgatg ttaggggtgg 360
ctgtcatctg cctgggagtt cgctatctgc aggtgtctcg gcagttccag gaggggacca 420
ggatttggga agccaccaat agcagcctgc agcagcagct cagggagaag ataagtcagc 480
tggggcagaa ggaggtggag cttcagaagg ctcggaaaga gctgatctcg agccaggaca 540
cattacagga gaagcagagg actcacgagg acgctgagca gcaactacaa gcctgccagg 600
ctgagagagc gaagaccaag gagaacctga aaactgagga ggagcggagg agggacctgg 660
accagaggtt gacaagcacg cgggagacac tgaggcgctt cttctctgat tcatcagaca 720
cctgctgtcc atgcggatgg attccatatc aggaaaggtg cttttacatc tcacataccc 780
teggaagtet ggaggagage caaaaataet geacatetet gteeteeaaa etggeageat 840
tegatgaacc ttctaagtat tactatgaag tttctctgcc cagcggctta gaggagttgc 900
tagategtte gaagteatat tggatacaga tgagcaagaa gtggaggcag gactetgaet 960
ctcaaagccg acattgtgtc aggataaaaa catattacca gaagtgggaa agaacaattt 1020
ccaagtgtgc agagetteac ecctgeattt gtgagtegga ggettteagg ttteetgatg 1080
ggatcaatct gaactgaaac ggacacttga acaagacctt gtgacctaca tccttaacct 1140
acggcctgcc aatttttaag actgctattc ctccagcact ccctcactct cgggcatgcc 1200
cagetaaggg atgacetget gettgettga aagetgetee agaaactgga ettetettgg 1260
gaagagtaaa gaagceteca gaaaagaett gacetteett aagaaettee caaactagag 1320
atgggtcagg ggagggc
<210> 7
<211> 359
<212> PRT
<213> Homo sapiens
<400> 7
Met Ala Glu Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Ala Pro
Leu Lys Lys Ser Ile Ser Ser Arg Leu Gly Gln Asp Pro Gly Ala Asp
                                                     30
                                 25
Asp Asp Gly Glu Ile Thr Tyr Glu Asn Val Gln Val Pro Ala Val Leu
Gly Val Pro Ser Ser Leu Ala Ser Ser Val Leu Gly Asp Lys Ala Ala
Val Lys Ser Glu Gln Pro Thr Ala Ser Trp Arg Ala Val Thr Ser Pro
Ala Val Gly Arg Ile Leu Pro Cys Arg Thr Thr Cys Leu Arg Tyr Leu
Leu Leu Gly Leu Leu Thr Cys Leu Leu Gly Val Thr Ala Ile
Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr
                            120
Asn Arg Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg
                        135
                                            140
```



Leu Lys Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser 150 Arg Arg Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg Ala His Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg 185 Gln Lys Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala 200 Leu Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Cys Pro Ser Gly Trp Ile Met His Gln Lys Ser Cys Phe Tyr Ile Ser Leu Thr Ser Lys Asn Trp Gln Glu 250 Ser Gln Lys Gln Cys Glu Thr Leu Ser Ser Lys Leu Ala Thr Phe Ser 260 265 Glu Ile Tyr Pro Gln Ser His Ser Tyr Tyr Phe Leu Asn Ser Leu Leu 280 Pro Asn Gly Gly Ser Gly Asn Ser Tyr Trp Thr Gly Leu Ser Ser Asn 295 Lys Asp Trp Lys Leu Thr Asp Asp Thr Gln Arg Thr Arg Thr Tyr Ala 315 Gln Ser Ser Lys Cys Asn Lys Val His Lys Thr Trp Ser Trp Trp Thr 330 Leu Glu Ser Glu Ser Cys Arg. Ser Ser Leu Pro Tyr Ile Cys Glu Met

Thr Ala Phe Arg Phe Pro Asp 355

<210> 8

<211> 1531

<212> DNA

<213> Homo sapiens

<400> 8

agtcacagag ggaacacaga gcctagttgt aaacggacag agacgagagg ggcaagggag 60 gacagtggat gacagggaag acgagtggg gcaagggag tcaggactgc tcaggaccat ggctgaggcc 120 atcacctatg cagatctgag gtttgtgaag gctcccctga agaagagcat ctccagccgg 180 ttaggacagg acccaggggc tgatgatgat ggggaaatca cctacgagaa tgttcaagtg 240 cccgcagtcc taggggtgcc ctcaagcttg gcttcttctg tactagggga caaagcagcg 300 gtcaagtcgg agcagccaac tgcgtcctgg agagccgtga cgtcaccagc tgtcggcgg 360 attctcccct gccgcacaac ctgcctgcga tacctcctgc tcggcctgct cctcacctgc 420 ctgctgttag gagtgaccgc catctgcctg ggagtgcgct atctgcaggt gtctcagcag 480



```
ctccagcaga cgaacagggt tctggaagtc actaacagca gcctgaggca gcagctccgc 540
ctcaagataa cgcagctggg acagagtgca gaggatctgc aggggtccag gagagagctg 600
qcqcaqaqtc aggaagcact acaggtggaa cagagggctc atcaggcggc cgaagggcag 660
ctacaggcct gccaggcaga cagacagaag acgaaggaga ccttgcaaag tgaggagcaa 720
cagaggaggg ccttggagca gaagctgagc aacatggaga acagactgaa gcccttcttc 780
acatgcggct cagcagacac ctgctgtccg tcgggatgga taatgcatca gaaaagctgc 840
ttttacatct cacttacttc aaaaaattgg caggagagcc aaaaacaatg tgaaactctg 900
tcttccaage tggccacatt cagtgaaatt tatccacaat cacactetta ctacttetta 960
aattcactgt tgccaaatgg tggttcaggg aattcatatt ggactggcct cagctctaac 1020
aaggattgga agttgactga tgatacacaa cgcactagga cttatgctca aagctcaaaa 1080
tgtaacaagg tacataaaac ttggtcatgg tggacactgg agtcagagtc atgtagaagt 1140
tetetteect acatetgtga gatgacaget tteaggttte cagattagga cagteetttg 1200
cactgagttg acactcatgc caacaagaac ctgtgcccct ccttcctaac ctgaggcctg 1260
gggttcctca gaccatctcc ttcattctgg gcagtgccag ccaccggctg acccacact 1320
gacactteca gecagtetge tgeetgetee etetteetga aactggaetg tteetgggaa 1380
aagggtgaag ccacctctag aagggacttt ggcctcccc caagaacttc ccatggtaga 1440
atggggtggg ggaggaggc gcacgggctg agcggatagg ggcggcccgg agccagccag 1500
gcagttttat tgaaatcttt ttaaataatt g
                                                                   1531
<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 9
                                                                   32
getgtegact gtgtgeeegt tgetgaagge et
<210> 10
<211> 53
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 10
```

gacggatect acttactttg ctttgcttgc ttgagataca ccgtcttctc tga

53